

SEQUENCE LISTING

<110> Merck & Co., Inc.
Steinkuhler, Christian
Lahm, Armin
Pallaoro, Michele
Nardella, Caterina

<120> SYNTHETIC HEPARANASE MOLECULES AND USES
THEREOF

<130> ITR0060Y-PCT

<150> 60/537,729
<151> 2004-01-20

<150> 60/506,479
<151> 2003-09-26

<160> 44

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<220>
<223> PCR primer

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<400> 2
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caggagcaat tg 72

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<212> PRT
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<220>
<223> Peptide

<400> 8
Trp Ala Phe Lys Asp Lys Pro Thr
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<210> 9
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 9
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gagcaattg 69

<210> 10
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide

<400> 10
Glu Gly Ser Gly Ser Glu Asn Leu Tyr Phe Gln Gly Ser Gly Gly
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<210> 11
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

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tac 63

<210> 12
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<212> PRT
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<220>
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<211> 66
<212> DNA
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acctac 66

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<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide

<400> 14
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Gln

<210> 15
<211> 74
<212> PRT
<213> Human

<400> 15
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Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn Leu Ala Thr
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Asp Pro Arg Phe Leu Ile Leu Gly Ser Pro Lys Leu Arg Thr Leu
35 40 45
Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr
50 55 60
Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu
65 70

<210> 16
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<212> PRT
<213> Human

<400> 16
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Ala Leu Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln
35 40 45
Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu
50 55 60
Leu Gly Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile
65 70 75 80
Asn Gly Ser Gln Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu
85 90 95
Arg Lys Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly
100 105 110
Gln Pro Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala
115 120 125
Gly Gly Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn
130 135 140
Gly Arg Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp
145 150 155 160
Ile Phe Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr
165 170 175
Arg Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly
180 185 190
Gly Gly Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp
195 200 205
Leu Asp Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met
210 215 220
Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn
225 230 235 240
Phe Asp Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu
245 250 255
Val Gly Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg
260 265 270
Lys Leu Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr
275 280 285
Lys Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr
290 295 300
Lys Tyr Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys

305	310	315	320
Tyr Leu Leu Arg Pro Leu Gly Pro His Gly	Leu Leu Ser Lys Ser Val		
325	330	335	
Gln Leu Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro			
340	345	350	
Pro Leu Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro			
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Ala Phe Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala			
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Cys Ile			
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<210> 17
 <211> 492
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hep 106

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Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro			
35	40	45	
Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn			
50	55	60	
Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu			
65	70	75	80
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly			
85	90	95	
Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Phe Lys Asn Ser			
100	105	110	
Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys			
115	120	125	
Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala			
130	135	140	
Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Asp Tyr Cys			
145	150	155	160
Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn			
165	170	175	
Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln Leu Gly			
180	185	190	
Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr Phe Lys			
195	200	205	
Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg Lys Thr			
210	215	220	
Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp			
225	230	235	240
Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg			
245	250	255	
Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val			
260	265	270	
Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val			
275	280	285	
Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala Pro Leu Leu			
290	295	300	
Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu			
305	310	315	320
Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe Gly			
325	330	335	

Ala	Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro	Leu	Pro	Asp
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Tyr	Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr	Lys	Val	Leu
		355				360					365				
Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg	Val	Tyr	Leu
		370				375				380					
His	Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly	Asp	Leu	Thr
	385			390					395					400	
Leu	Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu	Arg	Leu	Pro
								405		410				415	
Tyr	Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu	Arg	Pro	Leu
			420				425						430		
Gly	Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn	Gly	Leu	Thr
			435			440				445					
Leu	Lys	Met	Val	Asp	Asp	Gln	Thr	Leu	Pro	Pro	Leu	Met	Glu	Lys	Pro
			450			455				460					
Leu	Arg	Pro	Gly	Ser	Ser	Leu	Gly	Leu	Pro	Ala	Phe	Ser	Tyr	Ser	Phe
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<210> 18
<211> 1479
<212> DNA
<213> Artificial Sequence

<220>
<223> hep 106

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ctggacttct tcaccaggaa gcccgtgcac ctgtgtggcc cctcggttct gtcgcgtacc 180
attgacgcca acctggccac ggaccggcg ttcctcatcc tccctgggttcc tccaaagctt 240
cgtaccttgg ccaggaggctt tgctcctgtcg taccctgagggt ttgtggcacc aagacagac 300
ttcctaattt tcgatcccaa aaagttcaag aacagcacct ctgctcaggaa ctggacttga actcaagaag ctctgttagat 360
gtgctataca ctttgc当地 aatgcgttta 420
ttaagaacag cagatttgc当地 agttgctctt ggactactgc 480
tcttccaagg ggtataacat aacctaacag tttctttaag 540
aaggctgata tttcatcaa attttatcca attgcataaa 600
cttctaaagaa agttccaccc ttctgtatgt ttgtcagcc 660
cgaagaaaga cggctaaagat ctggaaacagt tctaattgtc ttcttggcctt 720
tcagttacat ggcattacta ctatgttggaa ctggcataatg ctaccaggaa agatttctt 780
aaccctgtat tattggacat ttttatttca tctgtgtccaa aagtttcca ggtgggtttag 840
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ctgtatgcca taaaccttcca taatgtcacc aagtacttgc gtttacccca tcccttttct 1260
aacaagcaag tggataaaaa ccttcttcaaga cctttggatc ctcatggatt actttccaaa 1320
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atggaaaaac ctctccggcc aggaagttca ctgggttgc cagttttctc atatagttt 1440
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<210> 19
<211> 1488
<212> DNA
<213> Artificial Sequence

<220>
<223> hep 109

<400> 19

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 attgacgccc acctggccac ggacccggcg tccctcatcc tcctgggttc tccaaagctt 240
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 tctgttagatg tgctatacac ttttgcacaa tgctcaggac tggacttgat ctttggccata 420
 aatgcgttat taagaacacgc agatttgcag tggaacagtt ctaatgctca gttgctcctg 480
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 ttccctaaga aggctgatgt ttcatcaat gggtcgcagt taggagaaga ttttattcaa 600
 ttgcataaaat ttctaaagaaa gtccacccctc aaaaatgcaa aactctatgg tcctgatgtt 660
 ggtcagccctc gaagaaaagac ggctaagatg ctgaagagct tcctgaaggc tggggagaa 720
 gtgattgatt cagttacatg gcatcactac tatttgaatg gacggactgc taccaggaa 780
 gattttctaa accctgatgtt attggacatt tttatccat ctgtcaaaaa agttttccag 840
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 ccaccccttaa tggaaaaacc tctccggccca ggaagttcac tgggcttgcc agctttctca 1440
 tatagtttt ttgtgataag aaatgcacaa gttgctgctt gcatctga 1488

<210> 20

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> hep 109

<400> 20

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Leu	His	Leu	Val	Ser	Pro	Ser	Phe	Leu	Ser	Val	Thr	Ile	Asp	Ala	Asn
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Leu	Ala	Thr	Asp	Pro	Arg	Phe	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	Leu
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Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	
								85		90			95		
Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Lys	Lys	Phe
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Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe
								115		120			125		
Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu
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Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu
								145		150			155		160
Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn
								165		170			175		
Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser
								180		185			190		
Gln	Leu	Gly	Glu	Asp	Phe	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser
								195		200			205		
Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg

210	215	220
Arg Lys Thr Ala Lys Met	Leu Lys Ser Phe Leu	Lys Ala Gly Gly Glu
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Val Ile Asp Ser Val Thr Trp His His	Tyr Tyr Leu Asn Gly Arg Thr	240
245	250	255
Ala Thr Arg Glu Asp Phe Leu Asn	Pro Asp Val Leu Asp Ile Phe Ile	
260	265	270
Ser Ser Val Gln Lys Val Phe Gln Val Val	Glu Ser Thr Arg Pro Gly	
275	280	285
Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala	Tyr Gly Gly Ala	
290	295	300
Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly	Phe Met Trp Leu Asp Lys	
305	310	315
Leu Gly Leu Ser Ala Arg Met Gly Ile	Glu Val Val Met Arg Gln Val	320
325	330	335
Phe Phe Gly Ala Gly Asn Tyr His	Leu Val Asp Glu Asn Phe Asp Pro	
340	345	350
Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys	Leu Val Gly Thr	
355	360	365
Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg	Arg Arg Lys Leu Arg	
370	375	380
Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro	Arg Tyr Lys Glu Gly	400
385	390	395
Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val	Thr Lys Tyr Leu	
405	410	415
Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys	Tyr Leu Leu	
420	425	430
Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser	Val Gln Leu Asn	
435	440	445
Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr	Leu Pro Pro Leu Met	
450	455	460
Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly	Leu Pro Ala Phe Ser	480
465	470	475
Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys	Ile	
485	490	495

<210> 21
 <211> 501
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hep GS3

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35 40 45
Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
50 55 60
Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65 70 75 80
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
85 90 95
Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Gly Ser Gly
100 105 110
Ser Gly Ser Lys Lys Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val
115 120 125
Asp Val Leu Tyr Thr Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe
130 135 140

Gly Leu Asn Ala Leu Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser
 145 150 155 160
 Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile
 165 170 175
 Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp
 180 185 190
 Ile Phe Ile Asn Gly Ser Gln Leu Gly Glu Asp Phe Ile Gln Leu His
 195 200 205
 Lys Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro
 210 215 220
 Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe
 225 230 235 240
 Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val Thr Trp His His Tyr
 245 250 255
 Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp
 260 265 270
 Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val Phe Gln Val Val
 275 280 285
 Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser
 290 295 300
 Ala Tyr Gly Gly Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly
 305 310 315 320
 Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu
 325 330 335
 Val Val Met Arg Gln Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val
 340 345 350
 Asp Glu Asn Phe Asp Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe
 355 360 365
 Lys Lys Leu Val Gly Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser
 370 375 380
 Lys Arg Arg Lys Leu Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn
 385 390 395 400
 Pro Arg Tyr Lys Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His
 405 410 415
 Asn Val Thr Lys Tyr Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln
 420 425 430
 Val Asp Lys Tyr Leu Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser
 435 440 445
 Lys Ser Val Gln Leu Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln
 450 455 460
 Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu
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 Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys
 485 490 495
 Val Ala Ala Cys Ile
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<210> 22
 <211> 1506
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hep GS3

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 aatgctcagt tgctcctgga ctactgcctc tccaaagggt ataacatttc ttggaaacta 540
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 caaatttctt ttggagcagg aactaccat ttatgtggatg aaaacttcga tccttaccc 1080
 gattattggc tatttcattt gttcaagaaa ttgttggca ccaagggtt aatggcaagc 1140
 gtcaggtt caaagagaag gaagcttgcg gtataccttcc atgcacaaa cactgacaat 1200
 ccaaggataa aagaaggaga tttactctg tatgccataa acctccataa tgtcaccaag 1260
 tacttgcgtt tacccatcc ttttctaaac aagcaagtgg ataaataacct tctaagaccc 1320
 ttgggaccc atggattact ttccaaatct gtccaactca atggtctaac tctaaagatg 1380
 gtggatgatc aaacccctgc acctttatg gaaaaaccc tccggccagg aagttcaactg 1440
 ggcttgcag ctttctata tagttttttt gtgataagaa atgccaatgt tgctgcttgc 1500
 atctga 1506

<210> 23
 <211> 1584
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hep GS4

<400> 23
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 ctgggtcccc tctccctgg cgcctgccc cgacctgcgc aagcacagga cgtcggtggac 120
 ctggacttct tcacccagga gcccgtgcac ctgtgagcc cctcggttccgt gtcgtcacc 180
 attgacgcca acctggccac ggaccggcgg ttccatcc tcctgggttc tccaaagctt 240
 cgtacctgg ccagaggctt gtctcctgcg tacctgaggt ttgggtggcac caagacagac 300
 ttccataattt tcgatcccaa gaaggaatca acctttgaag agagaagttt ctgggttca 360
 ggggcaggat cccgcggca atggccctac caggagcaat tgctactccg agaacactac 420
 cagaaaaatc tcaagaaacag caccactca agaagctcg tagatgtgtc atacaacttt 480
 gcaaaactgtc caggactgga ctgtatctt ggctaaatgg cgttattaaag aacagcagat 540
 ttgcgttggc acagttctaa tgctcagttt ctcctggact actgctttc caaggggtat 600
 aacatttctt gggaaactagg caatgaaccc aacagttcc ttaagaaggc tgatatttc 660
 atcaatgggt cgcgtttagg agaagatttt attcaattgc ataaactct aagaaagtcc 720
 accttcaaaaa atgcaaaact ctatggctt gatgttggc agcctcgaaag aaagacggct 780
 aagatgtga agagttccctt gaaaggctgtt ggagaagtga ttgattcagt tacatggcat 840
 cactactt tgaatggacg gactgttacc agggaaatgt ttctaaaccc tgatgttattg 900
 gacatttta ttcatctgt gcaaaaatgt ttccagggtgg ttgagagcac caggcctggc 960
 aagaaggctt ggttaggaga aacaagctct gcatatggag gcggagcggcc ttgtctatcc 1020
 gacacctttc cagctggctt tatgtggctg gataaattgg gcctgtcagc ccgaatggga 1080
 atagaagggtt tgatggggca agatttctt ggagcaggaa actaccattt agtggatgaa 1140
 aacttcgatc ctttacatgg tatttggcta tctttctgt tcaagaaattt ggtgggcacc 1200
 aagggtttaa tggcaagctg gcaagggttca aagagaagga agcttcgagt ataccttcat 1260
 tgcacaaaaca ctgacaatcc aaggatataaa gaaggagatt taactctgtt tgccataaac 1320
 ctccataatg tcaccaagta ctgtgggtt ccctatccctt tttctaaacaa gcaagtggat 1380
 aaatacccttca taagacctttt gggacccat ggttactttt ccaaattctgt ccaactcaat 1440
 ggtctacttca taaatgttgg ggtatgttca accttgcac cttaatggaa aaaaactctc 1500
 cggccaggaa gtttacttggg cttggccagct ttctcatata gttttttgtt gataagaaat 1560
 gccaaagggtt ctgttgcattt ctga 1584

<210> 24
 <211> 1524
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hep GS6

<400> 24
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ctgggtcccc tctccctgg cgcctgccc cgacactgcgc aagcacagga cgtcgtggac 120
ctggacttct tcacccagga gccgctgcac ctggtaggcc cctcggttct gtccgtcacc 180
attgacgcca acctggccac ggaccccgccg ttccatcc tcctgggttcc tccaaagctt 240
cgtaccttgg ccagaggctt gtctcctgcg tacctgaggt ttggggccac caagacagac 300
ttccatattt tcgatccaa agaggaaggt agcgggtccg gctctggtag cggctctgg 360
agcaaaaagt tcaagaacag cacctactca agaagctctg tagatgtgct atacacttt 420
gcaaactgct caggactgga ctgtatctt ggcctaaatg cgttattaag aacagcagat 480
ttgcagtgga acagttctaa tgctcagggt ctcctggact actgctcttc caaggggtat 540
aacatttctt gggaaactagg caatgaacct aacagttcc ttaagaaggc tgatatttc 600
atcaatgggt cgcgatggg agaagattt atcaatttc ataaaactt aagaaaagtcc 660
acccatccaaa atgcaaaaact ctatggtctt gtatgggtc agcctcgaag aaagacggct 720
aagatgctga agagcttcctt gaaggctgtt ggagaagtga ttgattcagt tacatggcat 780
caactactatt tgaatggacg gactgctacc agggaaagatt ttctaaaccc tgatgtattg 840
gacatttta ttcatctgt gcaaaaaagtt ttccaggtgg ttgagagcac caggcctggc 900
aagaaggctt ggttaggaga aacaagctct gcataatggag gcccggccg cttgtctatcc 960
gacacccctt cagctggctt tatgtggctt gataattgg gcctgtcagc ccgaatggga 1020
atagaatgg tgatgaggca agtattctt ggagcaggaa actaccattt agtggatgaa 1080
aacttcgatc ctttacctga ttatggctt tctcttctgt tcaagaaatt ggtgggcacc 1140
aagggtttaa tggcaagcgt gcaagggtca aagagaagga agcttcgagt ataccttcat 1200
tgcacaaaaca ctgacaaatcc aagggtataaa gaaggagatt taactctgtt tgccataaaac 1260
ctccataatg tcaccaagta ctgcgggtt ccctatcctt ttcttaacaa gcaagtggat 1320
aaatacccttc taagaccttt gggacccat ggattactt ccaaatctgtt ccaactcaat 1380
ggtctaactc taaaagatggt ggatgatcaa accttgccac cttaatggaa aaaacctctc 1440
cggccagggaa gttcactggg ctgcggact ttctcatata gttttttgt gataagaaat 1500
gccaaagttt ctgcggatctt ctga 1524

<210> 25
<211> 527
<212> PRT
<213> Artificial Sequence

<220>
<223> hep GS-A4

<400> 25
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1 5 10 15
Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
20 25 30
Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
35 40 45
Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
50 55 60
Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65 70 75 80
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
85 90 95
Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
100 105 110
Glu Glu Arg Ser Tyr Trp Gly Ser Gly Ala Gly Ser Gly Ala Glu Trp
115 120 125
Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
130 135 140
Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
145 150 155 160
Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
165 170 175
Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
180 185 190
Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
195 200 205

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
 210 215 220
 Gln Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser
 225 230 235 240
 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
 245 250 255
 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
 260 265 270
 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
 275 280 285
 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
 290 295 300
 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
 305 310 315 320
 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
 325 330 335
 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
 340 345 350
 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
 355 360 365
 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
 370 375 380
 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
 385 390 395 400
 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
 405 410 415
 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
 420 425 430
 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
 435 440 445
 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
 450 455 460
 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
 465 470 475 480
 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
 485 490 495
 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
 500 505 510
 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
 515 520 525

<210> 26
 <211> 507
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hep GS-A6

<400> 26
 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
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 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 20 25 30
 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
 35 40 45
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 50 55 60
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65 70 75 80
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Gly Ser Gly

Ser	Gly	Ser	100	Gly	Ser	Gly	Ser	105	Lys	Lys	Phe	Lys	Asn	Ser	Thr
			115				120				125				
Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe	Ala	Asn	Cys	Ser
			130				135			140					
Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu	Arg	Thr	Ala	Asp
			145				150			155					160
Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu	Asp	Tyr	Cys	Ser
			165				170			175					
Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn	Glu	Pro	Asn	Ser
			180				185			190					
Phe	Leu	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser	Gln	Leu	Gly	Glu	
			195				200			205					
Asp	Phe	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser	Thr	Phe	Lys	Asn
			210				215			220					
Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg	Arg	Lys	Thr	Ala
			225				230			235					240
Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu	Val	Ile	Asp	Ser
			245				250			255					
Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr	Ala	Thr	Arg	Glu
			260				265			270					
Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile	Ser	Ser	Val	Gln
			275				280			285					
Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly	Lys	Lys	Val	Trp
			290				295			300					
Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Gly	Ala	Pro	Leu	Leu	Ser
			305				310			315					320
Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys	Leu	Gly	Leu	Ser
			325				330			335					
Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val	Phe	Phe	Gly	Ala
			340				345			350					
Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro	Leu	Pro	Asp	Tyr
			355				360			365					
Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr	Lys	Val	Leu	Met
			370				375			380					
Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg	Val	Tyr	Leu	His
			385				390			395					400
Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly	Asp	Leu	Thr	Leu
			405				410			415					
Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu	Arg	Leu	Pro	Tyr
			420				425			430					
Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu	Arg	Pro	Leu	Gly
			435				440			445					
Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn	Gly	Leu	Thr	Leu
			450				455			460					
Lys	Met	Val	Asp	Asp	Gln	Thr	Leu	Pro	Pro	Leu	Met	Glu	Lys	Pro	Leu
			465				470			475					480
Arg	Pro	Gly	Ser	Ser	Leu	Gly	Leu	Pro	Ala	Phe	Ser	Tyr	Ser	Phe	Phe
			485				490			495					
Val	Ile	Arg	Asn	Ala	Lys	Val	Ala	Ala	Cys	Ile					
			500				505								

<210> 27
 <211> 526
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hep Hyal

<400> 27
 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
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Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 20 25 30
 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
 35 40 45
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 50 55 60
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65 70 75 80
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
 100 105 110
 Glu Glu Arg Ser Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Trp Pro
 115 120 125
 Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys
 130 135 140
 Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala
 145 150 155 160
 Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg
 165 170 175
 Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp
 180 185 190
 Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu
 195 200 205
 Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln
 210 215 220
 Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr
 225 230 235 240
 Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg
 245 250 255
 Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val
 260 265 270
 Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala
 275 280 285
 Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser
 290 295 300
 Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys
 305 310 315 320
 Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro
 325 330 335
 Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu
 340 345 350
 Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe
 355 360 365
 Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu
 370 375 380
 Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys
 385 390 395 400
 Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val
 405 410 415
 Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp
 420 425 430
 Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu Arg
 435 440 445
 Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu Arg
 450 455 460
 Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly
 465 470 475 480
 Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu
 485 490 495
 Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr
 500 505 510
 Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
 515 520 525

<210> 28
 <211> 1581
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hep Hyal

<400> 28
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 ctggacttct tcacccaggaa gccgctgcac ctggtgagcc cctcggttct gtccgtcacc 180
 attgacgcca acctggccac ggacccgggg ttccatcc tacctgaggt ttggtgccac caagacagac 300
 cgtacacctgg ccagaggctt gtctcctgcg tacctgaggt ttggtgccac caagacagac 300
 ttccataattt tcgatccaa gaaggaaatca acctttaaag agagaaggta ctgggccttc 360
 aaggacaaga cccccaatg gcccattacca gaggaaatgc tactccgaga acactaccag 420
 aaaaagtca agaacagcac ctactcaaga agctctgtag atgtgtata cactttgca 480
 aactgcttag gactggactt gatctttggc ctaaatgcgt tattaaagaa acgcagattt 540
 cagtggaaaca gttctaattgc tcagttgtct ctggactact gctcttccaa ggggtataac 600
 atttcttggg aactaggcaa tgaacctaacc agtttccatc agaaggctga tattttcatc 660
 aatgggtcgc agttaggaga agattttattt caatttgcata aacttctaaag aaagtccacc 720
 ttcaaaaatg caaaactcta tggtcctgtat gttggctcgc ctcgaagaaa gacggctaaag 780
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 tactatttga atggacggac tgcttaccagg gaagattttca taaaaccctga ttttgcac 900
 attttttattt catctgtgc aaaaattttc cagggtgggtt agagcaccag gcctggcaag 960
 aagggtctgtt taggagaaac aagctctgcata tatggaggcg gagcgcctt gctatccgac 1020
 acctttgcag ctggctttat gtggctgtat aaatttggcc tgcagcccg aatgggaata 1080
 gaagtgggtga tgaggcaagt attctttggc gcaggaaact accattttgtt ggtgaaaac 1140
 ttgcatctt tacctgttata ttggctatct cttctgttca agaaatttggt gggcaccaag 1200
 gtgttaatgg caagctgtca aggttcaaaag agaaggaaagc ttgcgttata ccttcattgc 1260
 acaaacaactg acaatccaaatgtataaagaa ggagatttaa ctctgtatgc cataaaaccc 1320
 cataatgtca ccaagtactt gcggttaccc tatccctttt ctaacaagca agtggataaa 1380
 taccttctaa gacccttggg acctcatgaa ttactttcca aatctgttca actcaatggt 1440
 ctaactctaa agatgggtga tgatcaaaacc ttggccaccc ttatggaaaa acctctccgg 1500
 ccaggaagtt cactgggtt ggcagcttcc tcataatagtt tttttgtgat aagaaatgcc 1560
 aaagttgtcgttgcatctga a 1581

<210> 29
 <211> 570
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hep TEV110-158

<400> 29
 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
 1 5 10 15
 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 20 25 30
 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
 35 40 45
 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 50 55 60
 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 65 70 75 80
 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 85 90 95
 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Gly Ser Gly
 100 105 110
 Ser Glu Asn Leu Tyr Phe Gln Gly Ser Gly Ser Thr Phe Glu Glu Arg
 115 120 125

Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly Ser
 130 135 140
 Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr Gln
 145 150 155 160
 Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Ser Gly Ser Gly Glu Asn
 165 170 175
 Leu Tyr Phe Gln Gly Ser Gly Ser Lys Lys Phe Lys Asn Ser Thr Tyr
 180 185 190
 Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn Cys Ser Gly
 195 200 205
 Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr Ala Asp Leu
 210 215 220
 Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu Asp Tyr Cys Ser Ser
 225 230 235 240
 Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn Glu Pro Asn Ser Phe
 245 250 255
 Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser Gln Leu Gly Glu Asp
 260 265 270
 Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala
 275 280 285
 Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys
 290 295 300
 Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val
 305 310 315 320
 Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp
 325 330 335
 Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys
 340 345 350
 Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu
 355 360 365
 Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser Asp
 370 375 380
 Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu Ser Ala
 385 390 395 400
 Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe Gly Ala Gly
 405 410 415
 Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu Pro Asp Tyr Trp
 420 425 430
 Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr Lys Val Leu Met Ala
 435 440 445
 Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg Val Tyr Leu His Cys
 450 455 460
 Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly Asp Leu Thr Leu Tyr
 465 470 475 480
 Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu Arg Leu Pro Tyr Pro
 485 490 495
 Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu Arg Pro Leu Gly Pro
 500 505 510
 His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn Gly Leu Thr Leu Lys
 515 520 525
 Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg
 530 535 540
 Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe Val
 545 550 555 560
 Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
 565 570

<210> 30
 <211> 1668
 <212> DNA
 <213> Artificial Sequence

<220>

<223> hep TEV110

<400> 30

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ctggactct	tcacccagg	gcccgtgcac	ctggtgagcc	cctcgttcct	gtccgtcacc	180
attgacgcca	acctggccac	ggaccccgccg	ttccatcc	tcctgggttc	tccaaagctt	240
cgtacctgg	ccagaggctt	gtctcctgcg	tacctgaggt	ttggtggcac	caagacagac	300
ttccataatt	tcgatccaa	gaaggaaggc	agcggatctg	agaacactgt	cttccagggt	360
tccggttcaa	ccttgaaga	gagaagttac	tggcaatctc	aagtcaacca	ggatatttgc	420
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gagcaatgc	tactccgaga	acactaccag	aaaaagttca	agaacagcac	ctactcaaga	540
agctctgtag	atgtgtct	cactttgc	aactgctcg	gactggactt	gatctttggc	600
ctaaatgcgt	tattaagaac	agcagatttgc	cagtggaaaca	gttctaattgc	tcagttgctc	660
ctggactact	gctcttccaa	ggggtataac	atttcttggg	aactaggcaa	tgaacctaac	720
agtttcccta	agaaggctga	tattttcatc	aatgggtcgc	agttaggaga	agattttatt	780
caattgcata	aacttctaag	aaagtccacc	ttcaaaaatg	caaaactcta	tggtcctgtat	840
gttggtcagc	ctcgaagaaa	gacggctcaag	atgtgtgaaga	gttccctgaa	ggctgggtgga	900
gaagtgtttg	attcagttac	atggcatcac	tactatttgc	atggacgac	tgctaccagg	960
gaagattttc	taaaaccctga	tgtattggac	atttttttttgc	catctgtgc	aaaagtttgc	1020
caggtgggtt	agagcaccag	gcctggcaag	aaggctgtgt	taggagaaac	aagctctgc	1080
tatggaggcg	gagcgcctt	gctatccgc	acctttgcag	ctggctttat	gtggctggat	1140
aaattgggcc	tgtcagcccg	aatgggaata	gaagtggta	tgaggcaagt	attctttgg	1200
gcaggaaact	accattttgt	ggatggaaaac	ttcgatcctt	tacctgttata	ttggctatct	1260
cttctgttca	agaaatttgc	gggcaccaag	gtgttaatgg	caagcgtgc	aggttcaaag	1320
agaaggaagc	ttcgagtata	ccttcatgc	acaaacactg	acaatccaa	gtataaaagaa	1380
ggagatttaa	ctctgtatgc	cataaacctc	cataatgtca	ccaagtactt	gcggttaccc	1440
tatccttttt	ctaacaagca	agtggataaa	tacccctaa	gacctttggg	acctcatg	1500
ttactttcca	aatctgtcca	actcaatgtt	ctaactctaa	agatgggtg	tgtcaaaacc	1560
ttgccaccc	taatggaaaa	acctctccgg	ccaggaagtt	cactgggtt	gccagcttgc	1620
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<210> 31

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> hep TEV110

<400> 31

Met	Leu	Leu	Arg	Ser	Lys	Pro	Ala	Leu	Pro	Pro	Pro	Leu	Met	Leu	Leu
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Leu	Leu	Gly	Pro	Leu	Gly	Pro	Leu	Ser	Pro	Gly	Ala	Leu	Pro	Arg	Pro
								20				25		30	
Ala	Gln	Ala	Gln	Asp	Val	Val	Asp	Leu	Asp	Phe	Phe	Thr	Gln	Glu	Pro
								35				40		45	
Leu	His	Leu	Val	Ser	Pro	Ser	Phe	Leu	Ser	Val	Thr	Ile	Asp	Ala	Asn
								50				55		60	
Leu	Ala	Thr	Asp	Pro	Arg	Phe	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	Leu
								65				70		75	
Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	Gly
								85				90		95	
Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Gly	Ser	Gly
								100				105		110	
Ser	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Ser	Gly	Ser	Thr	Phe	Glu	Glu	Arg
								115				120		125	
Ser	Tyr	Trp	Gln	Ser	Gln	Val	Asn	Gln	Asp	Ile	Cys	Lys	Tyr	Gly	Ser
								130				135		140	
Ile	Pro	Pro	Asp	Val	Glu	Glu	Lys	Leu	Arg	Leu	Glu	Trp	Pro	Tyr	Gln
								145				150		155	
Glu	Gln	Leu	Leu	Leu	Arg	Glu	His	Tyr	Gln	Lys	Lys	Phe	Lys	Asn	Ser
								165				170		175	
Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe	Ala	Asn	Cys

180	185	190													
Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	Leu	Arg	Thr	Ala
195				200				205							
Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	Leu	Asp	Tyr	Cys
210				215				220							
Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	Asn	Glu	Pro	Asn
225				230				235							240
Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser	Gln	Leu	Gly
	245				250				255						
Glu	Asp	Phe	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser	Thr	Phe	Lys
	260				265				270						
Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg	Arg	Lys	Thr
	275				280				285						
Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu	Val	Ile	Asp
	290				295				300						
Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr	Ala	Thr	Arg
305					310				315						320
Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile	Ser	Ser	Val
	325					330				335					
Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly	Lys	Lys	Val
	340					345				350					
Trp	Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Ala	Pro	Leu	Leu	
	355					360				365					
Ser	Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys	Leu	Gly	Leu
	370					375				380					
Ser	Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val	Phe	Phe	Gly
385					390				395						400
Ala	Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro	Leu	Pro	Asp
	405					410				415					
Tyr	Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr	Lys	Val	Leu
	420					425				430					
Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg	Val	Tyr	Leu
	435					440				445					
His	Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly	Asp	Leu	Thr
	450					455				460					
Leu	Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu	Arg	Leu	Pro
465					470				475						480
Tyr	Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu	Arg	Pro	Leu
	485					490				495					
Gly	Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn	Gly	Leu	Thr
	500					505				510					
Leu	Lys	Met	Val	Asp	Asp	Gln	Thr	Leu	Pro	Pro	Leu	Met	Glu	Lys	Pro
	515					520				525					
Leu	Arg	Pro	Gly	Ser	Ser	Leu	Gly	Leu	Pro	Ala	Phe	Ser	Tyr	Ser	Phe
	530					535				540					
Phe	Val	Ile	Arg	Asn	Ala	Lys	Val	Ala	Ala	Cys	Ile				
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<210> 32
 <211> 1710
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hep TEV110/158

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 ctggactct tcacccagga gccgctgcac ctggtgagcc cctcggttct gtcctgtcacc 180
 attgacgcca acctggccac ggacccgcgg ttccatcc tcctgggttc tccaaagctt 240
 cgtacctgg ccagaggctt gtctcctgcg taccctgaggt ttggtgccac caagacagac 300
 ttccataattt tcgatcccaa gaaggaaggc agcggatctg agaacctgta cttccagggt 360

tccgggttcaa	ccttgaaga	gagaagttac	tggcaatctc	aagtcaacca	ggatatttgc	420
aaatatggat	ccatccctcc	tgatgtggag	gagaagttac	gttggaaatg	gccctaccag	480
gagcaattgc	tactccgaga	acactaccag	tctggatccg	gtaaaaatct	ctattttcag	540
ggctcaggaa	gtaaaaaagt	caagaacagc	acctactcaa	gaagctctgt	agatgtgtca	600
tacactttg	caaactgctc	aggactggac	ttgatcttgc	gcttaatgc	gttattaaga	660
acagcagatt	tgcagtggaa	cagttctaat	gctcagttgc	tcctggacta	ctgtcttc	720
aagggttata	acattttcttg	ggaactaggc	aatgaaaccta	acagtttct	taagaaggct	780
gatatttca	tcaatgggtc	gcagtttagga	gaagatttta	ttcaatttgc	taaaacttcta	840
agaaaagtcca	ccttcaaaaaa	tgcaaaaactc	tatggtcctg	atgttggtca	gcctcgaaga	900
aagacggcta	agatgtctgaa	gagtttcctg	aaggctggtg	gagaagtgtat	tgattcagtt	960
acatggcattc	actactattt	gaatggacgg	actgctacca	ggaaagattt	tctaaacccct	1020
gatgtatgg	acatttttat	ttcatctgt	caaaaaagttt	tccagggtgt	tgagagcacc	1080
aggcctggca	agaaggctcg	gttaggagaa	acaagctctg	catatggagg	cggagcgc	1140
ttgttatccg	acaccccttgc	agctggctt	atgtggctgg	ataaaatttggg	cctgtcagcc	1200
cgaatggaa	tagaagtgg	gatgaggcaa	gtattctttg	gagcaggaaa	ctaccattta	1260
gtggatgaaa	acttcgatcc	tttacctgt	tattggctat	ctttctgtt	caagaaattg	1320
gtgggcacca	aggtgttaat	ggcaagcgtg	caaggttcaa	agagaaggaa	gcttcgagta	1380
taccttcatt	gcacaaaacac	tgacaatcca	aggataaaag	aaggagattt	aactctgtat	1440
gccataaacc	tcctataatgt	caccaagtac	ttgcgggtac	cctatccccc	ttcttacaacag	1500
caagtggata	aatactttct	aagaccccttgc	ggacccatcg	cttactttc	caaactctgtc	1560
caactcaatg	gtctactct	aaagatgtgt	gatgtacaa	ccttgcaccc	tttaatggaa	1620
aaacctctcc	ggccaggaaag	ttcaactgggc	ttgcgcaccc	tctcatatag	tttttttgg	1680
ataagaaaatg	ccaaagtgtc	tgcttgcatc				1710

<210> 33
<211> 174
<212> PRT
<213> Homo Sapiens

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<400> 33
Gln Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro Leu His
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Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn Leu Ala
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Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu Arg Thr
35 40 45
Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys
50 55 60
Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe Glu Glu
65 70 75 80
Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly
85 90 95
Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr
100 105 110
Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys Asn
115 120 125
Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe Ala Asn
130 135 140
Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr
145 150 155 160
Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
165 170

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<210> 34
<211> 174
<212> PRT
<213> Mus Musculus

<400> 34
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 Ser Val Ser Pro Ser Phe Leu Ser Ile Thr Ile Asp Ala Ser Leu Ala
 20 25 30

Thr Asp Pro Arg Phe Leu Thr Phe Leu Gly Ser Pro Arg Leu Arg Ala
 35 40 45
 Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys
 50 55 60
 Thr Asp Phe Leu Ile Phe Asp Pro Asp Lys Glu Pro Thr Ser Glu Glu
 65 70 75 80
 Arg Ser Tyr Trp Lys Ser Gln Val Asn His Asp Ile Cys Arg Ser Glu
 85 90 95
 Pro Val Ser Ala Ala Val Leu Arg Lys Leu Gln Val Glu Trp Pro Phe
 100 105 110
 Gln Glu Leu Leu Leu Arg Glu Gln Tyr Gln Lys Glu Phe Lys Asn
 115 120 125
 Ser Thr Tyr Ser Arg Ser Ser Val Asp Met Leu Tyr Ser Phe Ala Lys
 130 135 140
 Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu Arg Thr
 145 150 155 160
 Pro Asp Leu Arg Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
 165 170

<210> 35
 <211> 174
 <212> PRT
 <213> Bos taurus

<400> 35
 Ala Asp Asp Ala Ala Glu Leu Glu Phe Phe Thr Glu Arg Pro Leu His
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 Leu Val Ser Pro Ala Phe Leu Ser Phe Thr Ile Asp Ala Asn Leu Ala
 20 25 30
 Thr Asp Pro Arg Phe Phe Thr Phe Leu Gly Ser Ser Lys Leu Arg Thr
 35 40 45
 Leu Ala Arg Gly Leu Ala Pro Ala Tyr Leu Arg Phe Gly Gly Asn Lys
 50 55 60
 Gly Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Pro Ala Phe Glu Glu
 65 70 75 80
 Arg Ser Tyr Trp Leu Ser Gln Ser Asn Gln Asp Ile Cys Lys Ser Gly
 85 90 95
 Ser Ile Pro Ser Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Phe
 100 105 110
 Gln Glu Gln Val Leu Leu Arg Glu Gln Tyr Gln Lys Lys Phe Thr Asn
 115 120 125
 Ser Thr Tyr Ser Arg Ser Ser Val Asp Met Leu Tyr Thr Phe Ala Ser
 130 135 140
 Cys Ser Gly Leu Asn Leu Ile Phe Gly Val Asn Ala Leu Leu Arg Thr
 145 150 155 160
 Thr Asp Met His Trp Asp Ser Ser Asn Ala Gln Leu Leu Leu
 165 170

<210> 36
 <211> 173
 <212> PRT
 <213> Gallus Gallus

<400> 36
 Pro Arg Arg Thr Ala Glu Leu Gln Leu Gly Leu Arg Glu Pro Ile Gly
 1 5 10 15
 Ala Val Ser Pro Ala Phe Leu Ser Leu Thr Leu Asp Ala Ser Leu Ala
 20 25 30
 Arg Asp Pro Arg Phe Val Ala Leu Leu Arg His Pro Lys Leu His Thr
 35 40 45
 Leu Ala Ser Gly Leu Ser Pro Gly Phe Leu Arg Phe Gly Gly Thr Ser
 50 55 60

Thr Asp Phe Leu Ile Phe Asn Pro Asn Lys Asp Ser Thr Trp Glu Glu
 65 70 75 80
 Lys Val Leu Ser Glu Phe Gln Ala Lys Asp Val Cys Glu Ala Trp Pro
 85 90 95
 Ser Phe Ala Val Val Pro Lys Leu Leu Thr Gln Trp Pro Leu Gln
 100 105 110
 Glu Lys Leu Leu Ala Glu His Ser Trp Lys Lys His Lys Asn Thr
 115 120 125
 Thr Ile Thr Arg Ser Thr Leu Asp Ile Leu His Thr Phe Ala Ser Ser
 130 135 140
 Ser Gly Phe Arg Leu Val Phe Gly Leu Asn Ala Leu Leu Arg Arg Ala
 145 150 155 160
 Gly Leu Gln Trp Asp Ser Ser Asn Ala Lys Gln Leu Leu
 165 170

<210> 37
 <211> 189
 <212> PRT
 <213> Homo Sapiens

<400> 37
 Glu Lys Thr Leu Ile Leu Leu Asp Val Ser Thr Lys Asn Pro Val Arg
 1 5 10 15
 Thr Val Asn Glu Asn Phe Leu Ser Leu Gln Leu Asp Pro Ser Ile Ile
 20 25 30
 His Asp Gly Trp Leu Asp Phe Leu Ser Ser Lys Arg Leu Val Thr Leu
 35 40 45
 Ala Arg Gly Leu Ser Pro Ala Phe Leu Arg Phe Gly Gly Lys Arg Thr
 50 55 60
 Asp Phe Leu Gln Phe Gln Asn Leu Arg Asn Pro Ala Lys Ser Arg Gly
 65 70 75 80
 Gly Pro Gly Pro Asp Tyr Tyr Leu Lys Asn Tyr Glu Asp Asp Ile Val
 85 90 95
 Arg Ser Asp Val Ala Leu Asp Lys Gln Lys Gly Cys Lys Ile Ala Gln
 100 105 110
 His Pro Asp Val Met Leu Glu Leu Gln Arg Glu Lys Ala Ala Gln Met
 115 120 125
 His Leu Val Leu Leu Lys Glu Gln Phe Ser Asn Thr Tyr Ser Asn Leu
 130 135 140
 Ile Leu Thr Ala Arg Ser Leu Asp Lys Leu Tyr Asn Ser Ala Asp Cys
 145 150 155 160
 Ser Gly Leu His Leu Ile Phe Ala Leu Asn Ala Leu Arg Arg Asn Pro
 165 170 175
 Asn Asn Ser Trp Asn Ser Ser Ala Leu Ser Leu Leu
 180 185

<210> 38
 <211> 151
 <212> PRT
 <213> Bombyx Mori

<400> 38
 Val Arg Tyr Phe Val Thr Ile Asn Glu Asn Gln Glu Asp Ile Lys Leu
 1 5 10 15
 Ile Ser Glu Asp Phe Leu Ser Phe Gly Ile Asp Thr Ile Glu Ile Glu
 20 25 30
 Asn Tyr Asn Arg Ile Asn Tyr Ser Asp Thr Arg Leu Arg Glu Leu Ala
 35 40 45
 Ala Ala Leu Ser Pro Ala Arg Leu Arg Leu Gly Gly Thr Met Ser Glu
 50 55 60
 Arg Leu Ile Phe Ser Lys Glu Asn Ile Pro Ile Ser Cys His Asn Cys
 65 70 75 80

Ser Tyr Lys Ser Tyr Pro Lys Ser Leu Cys Gln Leu Ile Glu Lys Pro
 85 90 95
 Cys Lys His Lys His Lys Phe Leu Pro Phe Phe Ile Met Thr Gly Asn
 100 105 110
 Glu Trp Asn Gln Ile Asn Asp Phe Cys Arg Lys Thr Asn Leu Lys Leu
 115 120 125
 Leu Phe Ser Leu Asn Ala Met Leu Arg Asp Asn His Gly Trp Asn Glu
 130 135 140
 Lys Asn Ala Arg Glu Leu Ile
 145 150

<210> 39
 <211> 147
 <212> PRT
 <213> Hirudinaria manillensis

<400> 39
 Lys Asn Val Ile Ala Ser Val Ser Glu Ser Phe His Gly Val Ala Phe
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 Asp Ala Ser Leu Phe Ser Pro Lys Gly Pro Trp Ser Phe Val Asn Ile
 20 25 30
 Thr Ser Pro Lys Leu Phe Lys Leu Leu Glu Gly Leu Ser Pro Gly Tyr
 35 40 45
 Phe Arg Val Gly Gly Thr Phe Ala Asn Trp Leu Phe Asp Leu Asp
 50 55 60
 Glu Asn Asn Lys Trp Lys Asp Tyr Trp Ala Phe Lys Asp Lys Thr Pro
 65 70 75 80
 Glu Thr Ala Thr Ile Thr Arg Arg Trp Leu Phe Arg Lys Gln Asn Asn
 85 90 95
 Leu Lys Lys Glu Thr Phe Asp Asp Leu Val Lys Leu Thr Lys Gly Ser
 100 105 110
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 115 120 125
 Glu Ile Gly Lys Lys Thr Thr Ser Thr Trp Asp Ser Ser Glu Ala Glu
 130 135 140
 Lys Leu Phe
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<210> 40
 <211> 150
 <212> PRT
 <213> Scutellaria baicalensis

<400> 40
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 Tyr Gly Asn Cys Pro Trp Gly Lys Ser Ser Phe Leu Asn Leu Asp Leu
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 Asn Asn Asn Ile Ile Arg Asn Ala Val Lys Glu Phe Ala Pro Leu Lys
 35 40 45
 Leu Arg Phe Gly Gly Thr Leu Gln Asp Arg Leu Val Tyr Gln Thr Ser
 50 55 60
 Arg Asp Glu Pro Cys Asp Ser Thr Phe Tyr Asn Asn Thr Asn Leu Ile
 65 70 75 80
 Leu Asp Phe Ser His Ala Cys Leu Ser Leu Asp Arg Trp Asp Glu Ile
 85 90 95
 Asn Gln Phe Ile Leu Glu Thr Gly Ser Glu Ala Val Phe Gly Leu Asn
 100 105 110
 Ala Leu Arg Gly Lys Thr Val Glu Ile Lys Gly Ile Ile Lys Asp Gly
 115 120 125
 Gln Tyr Leu Gly Glu Thr Thr Ala Val Gly Glu Trp Asp Tyr Ser
 130 135 140

Asn Ser Lys Phe Leu Ile
145 150

<210> 41
<211> 138
<212> PRT
<213> *Arabidopsis thaliana*

<400> 41
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Tyr Asp Gln Cys Pro Trp Gly Tyr Ser Ser Val Ile Asn Met Asp Leu
20 25 30
Thr Arg Pro Leu Leu Thr Lys Ala Ile Lys Ala Phe Lys Pro Leu Arg
35 40 45
Ile Arg Ile Gly Gly Ser Leu Gln Asp Gln Val Ile Tyr Asp Val Gly
50 55 60
Asn Leu Lys Thr Pro Cys Arg Pro Phe Gln Lys Met Asn Ser Gly Leu
65 70 75 80
Phe Gly Phe Ser Lys Gly Cys Leu His Met Lys Arg Trp Asp Glu Leu
85 90 95
Asn Ser Phe Leu Thr Ala Thr Gly Ala Val Val Thr Phe Gly Leu Asn
100 105 110
Ala Leu Arg Gly Arg His Lys Leu Arg Gly Lys Ala Trp Gly Gly Ala
115 120 125
Trp Asp His Ile Asn Thr Gln Asp Phe Leu
130 135

<210> 42
<211> 138
<212> PRT
<213> *Arabidopsis thaliana*

<400> 42
Asp Phe Ile Cys Ala Thr Leu Asp Trp Trp Pro Pro Glu Lys Cys Asp
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Tyr Gly Ser Cys Ser Trp Asp His Ala Ser Ile Leu Asn Leu Asp Leu
20 25 30
Asn Asn Val Ile Leu Gln Asn Ala Ile Lys Ala Phe Ala Pro Leu Lys
35 40 45
Ile Arg Ile Gly Gly Thr Leu Gln Asp Ile Val Ile Tyr Glu Thr Pro
50 55 60
Asp Ser Lys Gln Pro Cys Leu Pro Phe Thr Lys Asn Ser Ser Ile Leu
65 70 75 80
Phe Gly Tyr Thr Gln Gly Cys Leu Pro Met Arg Arg Trp Asp Glu Leu
85 90 95
Asn Ala Phe Phe Arg Lys Thr Gly Thr Lys Val Ile Phe Gly Leu Asn
100 105 110
Ala Leu Ser Gly Arg Ser Ile Lys Ser Asn Gly Glu Ala Ile Gly Ala
115 120 125
Trp Asn Tyr Thr Asn Ala Glu Ser Phe Ile
130 135

<210> 43
<211> 138
<212> PRT
<213> *Arabidopsis thaliana*

<400> 43
Asn Phe Ile Cys Ala Thr Leu Asp Trp Trp Pro Pro Glu Lys Cys Asn
1 5 10 15

Tyr Asp Gln Cys Pro Trp Gly Tyr Ala Ser Leu Ile Asn Leu Asn Leu
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Ala Ser Pro Leu Leu Ala Lys Ala Ile Gln Ala Phe Arg Thr Leu Arg
35 40 45
Ile Arg Ile Gly Gly Ser Leu Gln Asp Gln Val Ile Tyr Asp Val Gly
50 55 60
Asp Leu Lys Thr Pro Cys Thr Gln Phe Lys Lys Thr Asp Asp Gly Leu
65 70 75 80
Phe Gly Phe Ser Glu Gly Cys Leu Tyr Met Lys Arg Trp Asp Glu Val
85 90 95
Asn His Phe Phe Asn Ala Thr Gly Ala Ile Val Thr Phe Gly Leu Asn
100 105 110
Ala Leu His Gly Arg Asn Lys Leu Asn Gly Thr Ala Trp Gly Gly Asp
115 120 125
Trp Asp His Thr Asn Thr Gln Asp Phe Met
130 135

<210> 44
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide

<400> 44
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